

06 May 2005

Alignment Results

Alignment: Global DNA alignment against reference molecule
Parameters: Scoring matrix: Linear (Mismatch 2, OpenGap 4, ExtGap 1)

Reference molecule: SEQIDNO:5, Region 1-1356

Number of sequences to align: 2

Settings: Similarity significance value cutoff: >= 60%



Summary of Percent Matches:

Reference: SEQIDNO:5 1 - 1356 (1356 bps) --
Sequence 2: Kimura Tri101 135 - 1490 (1356 bps) 99%

SEQIDNO:5 Kimura Tri10	1 atggcttcagaatacagctcgacaccctggccagctaccaggccttcgtatcac 135 atggcttcagaatacagctcgacaccctggccagctaccaggccttcgtatcac
SEQIDNO:5 Kimura Tri10	61 acccaaatacagtctcccttacccgtctgtatccctcaatatcccactattgtcagc 195 acccaaatacagtctcccttacccgtctgtatccctcaatatcccactattgtcagc
SEQIDNO:5 Kimura Tri10	121 accttcgagcaaggcttaagcgcttcgcgaagccgtcccatgggtcgccaggcagggtc 255 accttcgagcaaggcttaagcgcttcgcgaagccgtcccatgggtcgccaggcagggtc
SEQIDNO:5 Kimura Tri10	181 aaagccgagggcattagcgagggaaacacaggaacttccttatcgtccctttgaggac 315 aaagccgagggcattagcgagggaaacacaggaacttccttatcgtccctttgaggac
SEQIDNO:5 Kimura Tri10	241 gttccctcggttagtgaagacctccgcgtatccctcagccccacgatcgagggt 375 gttccctcggttagtgaagacctccgcgtatccctcagccccacgatcgagggt
SEQIDNO:5 Kimura Tri10	301 atgagaaaaggcgggataccctatggcgatgttgacgagaacatcatcgcccaaggaaag 435 atgagaaaaggcgggataccctatggcgatgttgacgagaacatcatcgcccaaggaaag
SEQIDNO:5 Kimura Tri10	361 acgttacctattggacctggtagtggccgcgtatccctcagccccacgatcgagggt 495 acgttacctattggacctggtagtggccgcgtatccctcagccccacgatcgagggt
SEQIDNO:5 Kimura Tri10	421 ctcaacttcatcaagggcggactcatccctactgtcaacggacacgacgggtctatggat 555 ctcaacttcatcaagggcggactcatccctactgtcaacggacacgacgggtctatggat
SEQIDNO:5 Kimura Tri10	481 atggtaggccaagatgcggtagccgtctactctccaaggcgtccgtaaacgaccattc 615 atggtaggccaagatgcggtagccgtctactctccaaggcgtccgtaaacgaccattc
SEQIDNO:5 Kimura Tri10	541 accgaagaggaaatgacggccatgaacctcgatcgcaagacgtatgttccattacatttt 675 accgaagaggaaatgacggccatgaacctcgatcgcaagacgtatgttccattacatttt
SEQIDNO:5 Kimura Tri10	601 aactatacgattggcccgaggtagatcatcagattgtcaaagctgtatgttagctgggt 735 aactacacgattggcccgaggtagatcatcagattgtcaaacattgtatgttagctgggt
SEQIDNO:5 Kimura Tri10	661 gacgctgttctcacgcggtagtgcgtggccgttccatcagccccaaaggcc 795 gacgctgttctcacgcggtagtgcgtggccgttccatcagccccaaaggcc
SEQIDNO:5 Kimura Tri10	721 atgtcagagctcaaggatgtctaccaaagactcttgcgtcaacaaatgtgttcgt 855 atgtcagagctcaaggatgtctaccaaagactcttgcgtcaacaaatgtgttcgt
SEQIDNO:5 Kimura Tri10	781 actgacgatgtcttcggcggtcatctggaaatcgcccttcgcgtgcgtcgaaaga 915 actgacgatgtcttcggcggtcatctggaaatcgcccttcgcgtgcgtcgaaaga
SEQIDNO:5 Kimura Tri10	841 atcgatggctctgcacctaccgaggtagttctggcggtctgttgcgtatgttcgt 975 atcgatggctctgcacctaccgaggtagttctggcggtctgttgcgtatgttcgt
SEQIDNO:5 Kimura Tri10	901 gtctcgaacaactaccaggccttcttcaaaaacatgacctaccacacaactcgaccatcgcc 1035 gtctcgaacaactaccaggccttcttcaaaaacatgacctaccacacaactcgaccatcgcc
SEQIDNO:5 Kimura Tri10	961 gaaatcgccaaacgagtcactcgccgcacagcatcagcccttcgttcgaaactcgaccc 1095 gaaatcgccaaacgagtcactcgccgcacagcatcagcccttcgttcgaaactcgaccc

SEQIDNO:5 1021 gcgagcatgcgccagcgaacaagaggctcgacgtacctgcacaacaaccccgacaag
Kimura Tri10 1155 gcgagcatgcgccagcgaacaagaggctcgacgtacctgcacaacaaccccgacaag

SEQIDNO:5 1081 tccaacgtatccctgacggctgatgcggaccatctaccagcgtcatgctgagttttgg
Kimura Tri10 1215 tccaacgtatctcgacggctgatgcggaccatctaccagcgtcatgctgagttttgg

SEQIDNO:5 1141 gccaaagggtggactctgggattacgactttggctcgactggtaagcccgagactgtg
Kimura Tri10 1275 gccaaaggctggactctgggattacgactttggctcgactggtaagcccgagactgtg

SEQIDNO:5 1201 agacggccaatcttgagcctgtttagagacttgcgttgcggatggaccgattgaaggcggat
Kimura Tri10 1335 agacggccaatcttgagcctgtttagagacttgcgttgcggatggaccgattgaaggcggat

SEQIDNO:5 1261 ggcgagttctgtgcggcgcttcttgaggatgaggatatggaccgattgaaggcggat
Kimura Tri10 1395 ggcgagttctgtgcggcgcttcttgaggatgaggatatggaccgattgaaggcggat

SEQIDNO:5 1321 aaggagttggaccaagtatgcgcagtacgttggtag
Kimura Tri10 1455 aaggagttggaccaagtatgcgcagtacgttggtag